



## SEQUENCE LISTING

<110> Frey et al.  
 <120> Polymerase Chimerae  
 <130> 4894  
 <140> US09/623,326  
 <141> 2001/02/08  
 <150> DE 198 10 879.6  
 <151> 1998-03-13  
 <160> 44  
 <170> PatentIn Ver. 2.1  
 <210> 1  
 <211> 2733  
 <212> DNA  
 <213> Artificial Sequence

RECEIVED  
 AUG 29 2001  
 TECH CENTER 1600/2900

<220>  
 <223> Description of Artificial Sequence: polynucleotide

<400> 1  
 atgaggggct cgcacacca tcaccatcac gctgctgacg atgacgataa aatgaggggc 60  
 atgctaccgc tatttgagcc caagggcccg gtcctcctgg tcgacggcca ccacctggcc 120  
 taccgcacct tccacgccct gaagggcctc accaccagcc ggggggagcc ggtgcaggcg 180  
 gtctacggct tcgccaagag cctcctcaag gccctcaagg aggacgggga cgcgggtgatc 240  
 gtggtctttg acgccaaggc cccctccttc cgccaagagg cctacggggg gtacaaggcg 300  
 ggccggggcc ccacgcggga ggactttccc cggaactcgc cctcatcaa ggagctggtg 360  
 gacctcctgg ggctggcgcg cctcgaggtc ccgggctacg aggcggacga cgtcctggcc 420  
 agcctggcca agaaggcgga aaaggagggc tacgagggtc gcacctcac cgccgacaaa 480  
 gacctttacc agctcctttc cgaccgcac cagctcctcc acccgagggt gtacctcatc 540  
 accccggcct ggctttggga aaagtacggc ctgaggcccg accagtgggc cgactaccgg 600  
 gccctgaccg gggacgagtc cgacaacctt cccgggggtc agggcatcgg ggagaagacg 660  
 gcgaggaagc ttctggagga gtgggggagc ctggaagccc tctcaagaa cctggaccgg 720  
 ctgaagcccg ccatccggga gaagatcctg gccacatgg acgatctgaa gctcctctgg 780  
 gacctggcca aggtgcgcac cgacctgccc ctggagggtg acttcgcca aaggcgggag 840  
 cccgaccggg agaggcttag ggcctttctg gagaggcttg agtttggcag cctcctccac 900  
 gagttcggcc ttctggaaag cccctatgac aactacgtca ccatccttga tgaagaaaca 960  
 ctgaaagcgt ggattgcgaa gctggaaaaa gcgcgggtat ttgcatattga taccgaaacc 1020  
 gacagccttg ataactctc tgctaacctg gtcgggcttt cttttgctat cgagccaggc 1080  
 gtagcggcat atattccggt tgctcatgat tatcttgatg cgcccgatca aatctctcgc 1140  
 gagcgtgcac tcgagttgct aaaaccgctg ctggaagatg aaaggcgct gaaggtcggg 1200  
 caaaacctga aatacgatcg cgggtattctg gcgaactacg gcattgaact gcgtgggatt 1260  
 gcgtttgata ccattgctgga gtcctacatt ctcaatagcg ttgccgggcg tcacgatatg 1320  
 gacagcctcg cggaacgttg gttgaagcac aaaaccatca cttttgaaga gattgctggt 1380  
 aaaggcaaaa atcaactgac ctttaaccag attgccctcg aagaagccgg acgttacgcc 1440  
 gccgaagatg cagatgtcac cttgcagttg catctgaaaa tgtggccgga tctgcaaaaa 1500  
 cagcagaggg tcctttggct ttaccgggag gtggagaggc ccttttcgc tgtcctggcc 1560  
 cacatggagg ccacgggggt gcgcctggac gtggcctatc tcagggcctt gtccctggag 1620  
 gtggccgagg aggtcgcccg cctcgaggcc gaggtcttcc gcctggccgg ccaccttctc 1680  
 aacctcaact cccgggacca gctggaaagg gtcccttttg acgagctagg gcttcccgcc 1740  
 atcggcaaga cggaagac cggaagcgc tccaccagcg ccgccgtcct ggaggccctc 1800  
 cgcgaggccc accccatcgt ggagaagatc ctgcagttac gggagctcac caagctgaag 1860  
 agcacctaca ttgacctt gcccagacct atccacccca ggacgggccc cctccacacc 1920  
 cgcttcaacc agacggccac ggccacgggc aggctaagta gctccgatcc caacctccag 1980  
 aacatccccg tccgcacccc gcttgggagc aggatccgcc gggccttcat cgccgaggag 2040

gggtggctat	tggtggccct	ggactatagc	cagatagagc	tcaggggtgct	ggcccacctc	2100
tccggcgacg	agaacctgat	ccgggtcttc	caggaggggc	gggacatcca	cacggagacc	2160
gccagctgga	tggtcggcgt	ccccgggag	gccgtggacc	ccctgatgcg	ccgggcggcc	2220
aagaccatca	acttcggggg	cctctacggc	atgtcggccc	accgcctctc	ccaggagcta	2280
gccatccctt	acgaggaggc	ccaggccttc	attgagcgct	actttcagag	cttccccaa	2340
gtgcgggcct	ggattgagaa	gaccctggag	gagggcagga	ggcgggggta	cgtggagacc	2400
ctcttcggcc	gccgccgcta	cgtgccagac	ctagaggccc	gggtgaagag	cgtgcgggag	2460
gcgggccgagc	gcatggcctt	caacatgccc	gtccagggca	ccgccgccga	cctcatgaag	2520
ctggctatgg	tgaagctctt	ccccaggctg	gaggaatgg	gggccaggat	gctccttcag	2580
gtccacgacg	agctggtcct	cgaggcccca	aaagagaggg	cggaggccgt	ggcccggctg	2640
gccaaaggagg	tcattggagg	ggtgtatccc	ctggccgtgc	ccctggaggt	ggaggtgggg	2700
ataggggagg	actggctctc	cgccaaggag	tga			2733

<210> 2

<211> 2733

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polynucleotide

<400> 2

atgaggggct	cgcataacca	tcaccatcac	gctgctgacg	atgacgataa	aatgaggggc	60
atgctaccgc	tattttagcc	caagggccgg	gtcctcctgg	tcgacggcca	ccacctggcc	120
taccgcacct	tccacgccct	gaagggcctc	accaccagcc	ggggggagcc	ggtgcaggcg	180
gtctacggct	tcgccaagag	cctcctcaag	gccctcaagg	aggacgggga	cgcggtgatc	240
gtggctctttg	acgccaaagg	cccctccttc	gccacagagg	cctacggggg	gtacaaggcg	300
ggccggggccc	ccacgccgga	ggactttccc	cggcaactcg	ccctcatcaa	ggagctggtg	360
gacctcctgg	ggctggcgcg	cctcgaggct	ccgggctacg	aggcggacga	cgtcctggcc	420
agcctggcca	agaaggcgga	aaaggagggg	tacgagggtc	gcatacctac	cgccgacaaa	480
gacctttacc	agctcctttc	cgaccgcata	cacgtcctcc	accccgaggg	gtacctcatc	540
accccgccct	ggctttggga	aaagtacggc	ctgaggcccg	accagtgggc	cgactaccgg	600
gccctgaccg	gggacgagtc	cgacaacctt	cccgggggtc	agggcacatc	ggagaagacg	660
gcgagggaagc	ttctgggagg	gtgggggagc	ctggaagccc	tcctcaagaa	cctggaccgg	720
ctgaagcccg	ccatccggga	gaagatcctg	gcccacatgg	acgatctgaa	gctctcctgg	780
gacctggcca	aggtgcgcac	cgacctgccc	ctggagggtg	acttcgccaa	aaggcgggag	840
cccgaccggg	agaggcttag	ggcctttctg	gagaggcttg	agtttggcag	cctcctccac	900
gagttcggcc	ttctggaaa	cccctatgac	aactacgtca	ccatccttga	tgaagaaa	960
ctgaaagcgt	ggattgcgaa	gctggaaaaa	gcgccgggtat	ttgcatttga	taccgaaacc	1020
gacagccttg	ataacatctc	tgctaacctg	gtcgggcttt	cttttgctat	cgagccaggc	1080
gtagcggcat	atattccggt	tgctcatgat	tatcttgatg	cgcccgatca	aatctctcgc	1140
gagcgtgcac	tcgagttgct	aaaaccgctg	ctggaagatg	aaaaggcgct	gaaggtcggg	1200
caaaacctga	aatacgatcg	cggtattctg	gcgaactacg	gcattgaact	gcgtgggatt	1260
gcgtttgata	ccatgctgga	gtcctacatt	ctcaatagcg	ttgccggggc	tcacgatatg	1320
gacagcctcg	cggaaacgtt	gttgaagcac	aaaaccatca	cttttgaaga	gattgctggt	1380
aaaggcaaaa	atcaactgac	ctttaaccag	attgccctcg	aagaagccgg	acgttacgcc	1440
gccgaagatg	cagatgtcac	cttgcaagtg	catctgaaaa	tgtggccgga	tctgcaaaaa	1500
cacaaagggc	cgttgaacgt	cttcgagaat	atcgaaatgc	cgtggtgccc	ggtgctttca	1560
cgcattgaac	gtaacgggtg	gcgctgggac	gtggcctatc	tcagggcctt	gtccctggag	1620
gtggccgagg	agatcgcccc	cctcgaggcc	gaggtcttcc	gcctggccgg	ccacctcttc	1680
aacctcaact	cccgggacca	gctggaaaag	gtcctctttg	acgagctagg	gcttcccgcc	1740
atcggaaga	cggagaagac	cggcaagcgc	tccaccagcg	ccgccgtcct	ggaggccctc	1800
cgcgaggccc	accccatcgt	ggagaagatc	ctgcagtacc	gggagctcac	caagctgaag	1860
agcacctaca	ttgacctctt	gccggacctc	atccacccca	ggacggggcc	cctccacacc	1920
cgcttcaacc	agacggccac	ggccacgggc	aggctaagta	gctccgatcc	caacctccag	1980
aacatccccg	tccgcacccc	gcttgggcag	aggtatccgc	gggccttcat	cgccgaggag	2040
gggtggctat	tggtggccct	ggactatagc	cagatagagc	tcaggggtgct	ggcccacctc	2100
tccggcgacg	agaacctgat	ccgggtcttc	caggaggggc	gggacatcca	cacggagacc	2160
gccagctgga	tggtcggcgt	ccccgggag	gccgtggacc	ccctgatgcg	ccgggcggcc	2220
aagaccatca	acttcggggg	cctctacggc	atgtcggccc	accgcctctc	ccaggagcta	2280
gccatccctt	acgaggaggc	ccaggccttc	attgagcgct	actttcagag	cttccccaa	2340
gtgcgggcct	ggattgagaa	gaccctggag	gagggcagga	ggcgggggta	cgtggagacc	2400

ctcttcggcc	gccgccgcta	cgtgccagac	ctagaggccc	gggtgaagag	cgtgcgggag	2460
gcgcccgagc	gcatggcctt	caacatgccc	gtccaggggca	ccgccgccga	cctcatgaag	2520
ctggctatgg	tgaagctctt	ccccaggctg	gaggaaatgg	gggccaggat	gctccttcag	2580
gtccacgacg	agctggctct	cgaggcccca	aaagagaggg	cggaggccgt	ggccccgctg	2640
gccaaggagg	tcatggaggg	ggtgtatccc	ctggccgtgc	ccctggaggt	ggaggtgggg	2700
ataggggagg	actggctctc	cgccaaggag	tga			2733

<210> 3

<211> 2727

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polynucleotide

<400> 3

atgaggggct	cgcataacca	tcaccatcac	gctgctgacg	atgacgataa	aatgaggggc	60
atgctaccgc	tatttgagcc	caagggccgg	gtcctcctgg	tcgacggcca	ccacctggcc	120
taccgcacct	tccacgccct	gaagggcctc	accaccagcc	ggggggagcc	ggtgcaggcg	180
gtctacggct	tcgccaaagag	cctcctcaag	gccctcaagg	aggacgggga	cgcggtgatc	240
gtggtccttg	acgccaaagg	ccccctcttc	cgccacgagg	cctacggggg	gtacaaggcg	300
ggccggggccc	ccacgccgga	ggacttttccc	cgccaactcg	ccctcatcaa	ggagctgggtg	360
gacctcctgg	ggctggcgcg	cctcgaggtc	ccgggctacg	aggcggacga	cgtcctggcc	420
agcctggcca	agaaggcgga	aaaggagggc	tacgaggtcc	gcatacctcac	cgccgacaaa	480
gacctttacc	agctcctttc	cgaccgcatac	cacgtcctcc	accccgaggg	gtacctcatc	540
acccggcctt	ggctttggga	aaagtacggc	ctgaggcccg	accagtgggc	cgactaccgg	600
gccctgaccg	gggacgagtc	cgacaacctt	cccgggggtca	agggcatcgg	ggagaagacg	660
gcgaggaagc	ttctggagga	gtgggggagc	ctggaagccc	tcctcaagaa	cctggaccgg	720
ctgaagcccg	ccatccggga	gaagatcctg	gcccacatgg	acgatctgaa	gctctcctgg	780
gacctggcca	aggtgcgcac	cgacctgccc	ctggaggtgg	acttcgcca	aaggcggggg	840
cccgcaccgg	agaggcttag	ggcctttctg	gagaggcttg	agtttggcag	cctcctccac	900
gagttcggcc	ttctggaaag	cccccccggt	ggatacagaa	tagtgaaaga	cctgggtgga	960
tttgaaaaaac	tcataagaaa	actgagagaa	tccccttcgt	tcgccataga	tcttgagacg	1020
tcttccctcg	atccttttga	ctgcgacatt	gtcggatatc	ctgtgtcttt	caaaccaaaag	1080
gaagcgtact	acataccact	ccatcataga	aacgcccaga	acctggatga	aaaagaagtt	1140
ctgaaaaagc	taaaagaaat	cctggaggac	cccggagcaa	agatcggttg	tcagaatttg	1200
aaattcgatt	acaagggtgt	gatggtaaag	ggtgttgaa	ctgtccctcc	tcacttcgac	1260
acgatgatag	cggttacctt	tcttgagcga	aacgaaaaga	agttcaatct	ggacgatctc	1320
gcattgaaat	ttcttggaat	caaaatgacc	tcttaccagg	aactcatgtc	cttctcttct	1380
ccgctgtttg	gttttcagtt	tgcgatgtt	cctgtagaaa	aagcagcgaa	ctattcctgt	1440
gaagatgccg	acatcaccta	cagactctac	aagatcctga	gcttaaaact	ccacgaggag	1500
aggctccttt	ggctttaccg	ggaggtggag	aggccccctt	ccgctgtcct	ggcccatg	1560
gaggccacgg	gggtgcgcct	ggacgtggcc	tatctcaggg	ccttgctcct	ggaggtggcc	1620
gaggagatcg	ccgcctcgca	ggccgaggtc	ttccgcctgg	ccggccaccc	cttcaacctc	1680
aactcccggg	accagctgga	aaagggtcct	tttgacgagc	tagggcttcc	cgccatcggc	1740
aagacggaga	agaccggcaa	gcgctccacc	agcgcgcgg	tcctggaggc	cctccgcgag	1800
gcccacccca	tcgtggagaa	gatcctgcag	taccgggagc	tcaccaagct	gaagagcacc	1860
tacattgacc	ccttgccgga	cctcatccac	cccaggacgg	gccgcctcca	caccgcttc	1920
aaccagacgg	ccacggccac	gggcaggcta	agtagctccg	atcccaacct	ccagaacatc	1980
cccgtccgca	ccccgcttgg	gcagaggatc	cgccgggcct	tcatacgccga	ggaggggtgg	2040
ctattgggtg	ccctggacta	tagccagata	gagctcaggg	tgctggccca	cctctccggc	2100
gacgagaacc	tgatccgggt	cttccaggag	gggcgggaca	tcacacgga	gaccgccagc	2160
tggatgttcg	gcgtcccccg	ggaggccgtg	gacccctga	tgcgcggggc	ggccaagacc	2220
atcaacttcg	gggtcctcta	cggcatgtcg	gcccaccgcc	tctcccagga	gtagccatc	2280
ccttacgagg	aggcccaggc	cttcattgag	cgctactttc	agagcttccc	caagggtcgg	2340
gcctggattg	agaagaccct	ggaggagggc	aggaggcggg	ggtacgtgga	gaccctcttc	2400
ggccgcccgc	gctacgtgcc	agacctagag	gcccgggtga	agagcgtgcg	ggaggcggcc	2460
gagcgcattg	ccttcaacat	gcccgtccag	ggcaccgccc	ccgacctcat	gaagctggct	2520
atggtgaagc	tcttccccag	gctggaggaa	atgggggcca	ggatgctcct	tcaggtccac	2580
gacgagctgg	tcctcgaggc	cccaaaagag	agggcggagg	ccgtggcccc	gctggccaag	2640
gaggtcatgg	aggggggtga	tccccgtggc	gtgcccctgg	aggtggaggt	ggggataggg	2700
gaggactggc	tctccgccaa	ggagtga				2727

<210> 4  
 <211> 2727  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: polynucleotide

```
<400> 4
atgaggggct cgcatacaca tcaccatcac gctgctgacg atgacgataa aatgaggggc 60
atgctaccgc tatgtgagcc caagggcccg gtcctcctgg tcgacggcca ccacctggcc 120
taccgcacct tccacgccct gaagggcctc accaccagcc gggggggagcc ggtgcaggcg 180
gtctacggct tcgccaagag cctcctcaag gccctcaagg aggacgggga cgcggtgatc 240
gtggtctttg acgccaaggc cccctccttc cgccacgagg cctacggggg gtacaaggcg 300
ggccggggcc ccacgccgga ggactttccc cggcaactcg ccctcatcaa ggagctgggtg 360
gacctcctgg ggctggcgcg cctcgaggct ccgggctacg aggcggacga cgtcctggcc 420
agcctggcca agaaggcgga aaaggagggc tacgaggtcc gcatacctcac cgccgacaaa 480
gacctttacc agctcctttc cgaccgcata cacgtcctcc accccgaggg gtacctcatc 540
accccgccct ggctttggga aaagtacggc ctgaggcccg accagtgggc cgactaccgg 600
gccctgaccg gggacgagtc cgacaacctt ccgggggtca agggcatcgg ggagaagacg 660
gcgaggaagc ttctggagga gtgggggagc ctggaagccc tcctcaagaa cctggaccgg 720
ctgaagcccg ccatccggga gaagatcctg gccacatgg acgatctgaa gctctcctgg 780
gacctggcca aggtgcgcac cgacctgccc ctggaggtgg acttcgccaa aaggcgggag 840
cccgaccggg agaggcttag ggcctttctg gagaggcttg agtttggcag cctcctccac 900
gagttcggcc ttctggaaag ccccccggtt ggatacagaa tagtgaaaga cctggtggaa 960
tttgaaaaac tcatagagaa actgagagaa tccccttcgt tcgccataga tcttgagacg 1020
tcttccctcg atcctttcga ctgcgacatt gtcggtatct ctgtgtcttt caaaccaaag 1080
gaagcgtact acataccact ccatcataga aacgcccaga acctggatga aaaagaagtt 1140
ctgaaaaagc taaaagaaat cctggaggac ccgggagcaa agatcgttgg tcagaatttg 1200
aaattcgatt acaaggtggt gatggtaaag ggtgttgaaac ctgtccctcc tcacttcgac 1260
acgatgatag cggcttacct tcttgagccg aacgaaaaga agttcaatct ggacgatctc 1320
gcattgaaat ttcttgata caaaatgacc tcttaccagg aactcatgtc cttctcttct 1380
ccgctgtttg gtttcagttt tgccgatgtt cctgtagaaa aagcagcgaa ctattcctgt 1440
gaagatgcag acatcaccta cagactctac aagatcctga gcttaaaact ccacgaggca 1500
gatctggaga acgtgttcta caagatagaa atgcctcttg tgagcgtgct tgcacggatg 1560
gaactgaacg gtgtgcccct ggacgtggcc tatctcaggg ccttgctccc ggaggtggcc 1620
gaggagatcg ccgcctcga ggccgaggtc ttccgcctgg ccggccaccc cttcaacctc 1680
aactcccggg accagctgga aagggtcctc agcgcgcccg tctggaggc cctccgcgag 1800
aagacggaga agaccggcaa gcgctctacc agcgcgcccg tcaccaagct gaagagcacc 1860
gcccacccca tcgtggagaa gatcctgcag taccgggagc tcaccaagct caccgcctcca 1920
tacattgacc ccttgccgga cctcatccac ccagggacgg gccgcctcca atcccaacct ccagaacatc 1980
aaccagacgg ccacggccac gggcaggcta agtagctccg atcccaacct ccagaacatc 2040
cccgtccgca ccccgcttgg gcagaggatc cgccgggcct tcatacgccga ggaggggtgg 2100
ctattggtgg ccttgacta tagccagata gagctcaggg tgctggccca cctctccggc 2160
gacgagaacc tgatccgggt cttccaggag gggcgggaca tccacacgga gaccgccagc 2220
tggtgttcg gcgtcccccg ggaggccgtg gacccctga tgcgccgggc ggccaagacc 2280
atcaacttcg ggttcctcta cggcatgtcg gccaccgccc tctcccagga gctagccatc 2340
ccttacgagg agggccaggc cttcatttag cgtaactttc agagcttccc caaggtgcgg 2400
gcctggattg agaagacctt ggaggagggc aggagggcgg ggtacgtgga gaccctcttc 2460
ggccgcccgc gctacgtgcc agacctagag gcccggtgga agagcgtgcg ggaggcgccc 2520
gagcgcattg ccttcaacat gcccgtccag ggcaccgccc cggacctcat gaagctggct 2580
atggtgaagc tcttccccag gctggaggaa atggggggcca ggatgctcct tcaggtccac 2640
gacgagctgg tcctcgaggc cccaaaagag agggcgagg ccgtggcccc gctggccaag 2700
gaggtcatgg agggggtgta tcccctggcc gtgcccctgg aggtggagggt ggggataggg 2727
gaggactggc tctccgcaa ggagtga
```

<210> 5  
 <211> 2850  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polynucleotide

```
<400> 5
atgagggggt cgcatacaca tcaccatcac gctgctgacg atgacgataa aatgaggggc 60
atgtacacgc tatttgagcc caagggcccg gtcctcctgg tcgacggcca ccacctggcc 120
taccgcacct tccacgcctt gaagggcctc accaccagcc ggggggagcc ggtgcaggcg 180
gtctacggct tcgccaagag cctcctcaag gccctcaagg aggacgggga cgcggtgatc 240
gtggtctttg acgccaaggg cccctccttc cgccacgagg cctacggggg gtacaaggcg 300
ggccggggccc ccacgcggga ggactttccc cggcaactcg ccctcatcaa ggagctggtg 360
gacctcctgg ggctggcgcg cctcgaggtc ccgggctacg aggcggacga cgtcctggcc 420
agcctggcca agaaggcgga aaaggagggc tacgaggtcc gcatcctcac cgccgacaaa 480
gacctttacc agctcctttc cgaccgcac cagtcctcc accccgaggg gtacctcatc 540
accccgccct ggctttggga aaagtacggc ctgaggcccc accagtgggc cgactaccgg 600
gccctgacgg gggacgagtc cgacaacctt cccggggtca agggcatcgg ggagaagacg 660
gagaggaagc ttctggagga gtgggggagc ctggaagccc tcctcaagaa cctggaccgg 720
ctgaagcccc ccacccggga gaagatcctg gcccacatgg acgatctgaa gctctcctgg 780
gacctggcca aggtgcgcac gacctgccc ctggagggtg acttcgcca aaggcgggag 840
cccggccggg agaggcttag ggctttctg gagaggcttg agtttgccag cctcctccac 900
gagttcggcc ttctggaaag ccccatcca gcagttgtg acatcttcca atacgatatt 960
ccatttgcaa agagatacct catcgacaaa ggcctaatac caatggaggg ggaagaagag 1020
ctaaagattc ttgccttcga tatagaaacc ctctatcacg aaggagaaga gtttgaaaaa 1080
ggcccaatta taatgattag ttatgcagat gaaaatgaag caaaggatgat tacttgaaaa 1140
aacatagatc ttccatacgt tgaggttgta tcaagcgaga gagagatgat aaagagattt 1200
ctcaggatta tcagggagaa ggatcctgac attatagtta cttataatgg agactcattc 1260
gacttcccat atttagcgaa aagggcagaa aaacttgagg ttaaattaac cattggaaag 1320
gatggaagcg agcccaagat gcagagaata ggcgatatga cggctgtaga agtcaaggga 1380
agaatacatt tcgacttgta tcatgtaata acaaggacaa taaatctccc aacatacaca 1440
ctagaggctg tatatgaagc aatttttgga aagccaaagg agaaggtata cgccgaccgag 1500
atagcaaaag cctgggaaag tggagagaac cttgagagag ttgccaaata ctcgatggaa 1560
gatgcaaagg caacttatga actcgggaaa gaattccttc caatggaaat tcagctttca 1620
gagaggctcc tttggcttta ccgggagggt gagaggcccc tttccgctgt cctggagggtg 1740
atggaggcca cgggggtgcg cctggacgtg gcttatctca gggccttgct cctggagggtg 1740
gccgaggaga tcgcccgcct cgaggccgag ctctttgacg agctagggtt tcccgccatc 1860
ctcaactccc gggaccagct ggaaagggtc ctctttgacg agctagggtt tcccgccatc 1860
ggcaagacgg agaagaccgg caagcgctcc accagcgccg ccgtcctgga ggccctccgc 1920
gaggccacc ccacgtgga gaagatcctg cagtagccgg agctcaccaa gctgaagagc 1980
acctacattg accccttgcc ggacctcatc caccacagga cgggcccgcct ccacaccgc 2040
ttcaaccaga cggccacggc caggggcagg ctaagtagct ccgatcccaa cctccagaac 2100
atccccgtcc gcacccgct tgggcagagg atccgcggg ccttcacgct cgaggagggg 2160
tggctattgg tggccctgga ctatagccag atagagctca ggggtgctgg ccacctctcc 2220
ggcgacgaga acctgatccg ggtcttccag gaggggcccg acatccacac ggagaccgcc 2280
agctggatgt tcggcgctcc ccgggaggcc gtggaccccc tgatgcgcgg ggcggccaag 2340
accatcaact tcggggctct ctacggcatg tcggcccacc gctctcccca ggagctagcc 2400
atcccttacg aggaggccca ggccttcatt gagcgtact ttcagagctt ccccaagggtg 2460
cgggcctgga ttgagaagac cctggaggag ggcaggaggg gggggtacgt ggagaccctc 2520
ttcgcccgcc gccgctacgt gccagaccta gagggccggg tgaagagcgt gcgggaggcg 2580
gccgagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctg 2640
gctatggtga agctcttccc caggctggag gaaatggggg ccaggatgct ccttcaggtc 2700
cacgacgagc tggctcctga ggcccaaaa gagaggcggg aggccgtggc ccggtggcc 2760
aaggaggtca tggagggggg gtatccccct gccgtgcccc tggaggtgga ggtggggata 2820
ggggaggact ggctctccgc caaggagtga 2850
```

<210> 6

<211> 2949

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polynucleotide

<400> 6

```
atgagggggt cgcatacaca tcaccatcac gctgctgacg atgacgataa aatgaggggc 60
```

```

atgctaccgc tatttgagcc caagggccgg gtcctcctgg tcgacggcca ccacctggcc 120
taccgcacct tccacgccct gaagggccctc accaccagcc ggggggagcc ggtgcaggcg 180
gtctacggct tcgccaagag cctcctcaag gccctcaagg aggacgggga cgcggtgatc 240
gtgggtctttg acgccaaggg cccctccttc cgccacgagg cctacggggg gtacaaggcg 300
ggccggggccc ccacgccgga ggactttccc cggcaactcg ccctcatcaa ggagctgggtg 360
gacctcctgg ggctggcgcg cctcgaggtc ccgggctacg agggcgacga cgtcctggcc 420
agcctggcca agaaggcgga aaaggagggc tacgagggtcc gcctcctcac cgccgacaaa 480
gacctttacc agctcctttc cgaccgcac cagtcctcc acccgaggg gtacctcatc 540
accccgccct ggctttggga aaagtacggc ctgaggcccc accagtgggc cgactaccgg 600
gccctgaccg gggacgagtc cgacaacctt cccggggtca agggcatcgg ggagaagacg 660
gcgagggaagc ttctggagga gtgggggagc ctggaagccc tcctcaagaa cctggaccgg 720
ctgaagcccc ccatccggga gaagatcctg gccacatgg acgatctgaa gctctcctgg 780
gacctggcca aggtgcgcac cgacctgccc ctggagggtg acttcgcaa aaggcgggag 840
cccgaccggg agaggcttag ggctttctg gagaggcttg agtttggcag cctcctccac 900
gagttcgccc ttctggaaa cccggttaga gaacatccag cagttgtgga catcttcgaa 960
tacgatattc catttgcaaa gagatacctc atcgacaaa gcctaatacc aatggagggg 1020
gaagaagagc taaagattct tgccttcgat atagaaaccc tctatcacga aggagaagag 1080
tttgaaaaag gcccaattat aatgattagt tatgcagatg aaaatgaagc aaagggtgatt 1140
acttgaaaaa acatagatct tccatacgtt gaggttgtat caagcgagag agagatgata 1200
aagagatttc tcaggattat cagggagaag gatcctgaca ttatagttac ttataatgga 1260
gactcattcg acttcccata tttagcgaaa agggcagaaa aacttgggat taaattaacc 1320
attggaagag atggaagcga gcccaagatg cagagaatag gcgatatgac ggctgtagaa 1380
gtcaaggga gaatacattt cgacttgtat catgtaataa caaggacaat aaatctccca 1440
acatacacac tagaggctgt atatgaagca atttttggaa agccaaagga gaaggtatac 1500
gccgacgaga tagcaaaagc ctgggaaagt ggagagaacc ttgagagagt tgccaaatac 1560
tcgatggaag atgcaaaggc aacttatgaa ctcgggaaaag aattccttcc aatggaaatt 1620
cagctttcaa gattagttgg acaaccttta tgggtgttt caaggtcaag cacagggaac 1680
cttgtagagt ggttcttact taggaaagcc tacgaaagaa acgaagtagc tccaaacaag 1740
ccaagtgaag aggagtatca aagaaggctc agggagagct acacagggtg attcgtgcgc 1800
ctggacgtgg cctatctcag ggccttgtcc ctggagggtg ccgaggagat cgcccgccct 1860
gaggccgagg tcttcgcctt ggccggccac cccttcaacc tcaactccc ggaaccagt 1920
gaaaggggtc cctttgacga gctagggtct cccgccatcg gcaagacgga gaagaccggc 1980
aagcgctcca ccagcccgcc cgctctggag gccctccgag agggccaccc catcgtggag 2040
aagatcctgc agtaccggga gctcaccaag ctgaagagca cctacattga ccccttgccg 2100
gacctcatcc accccaggac gggccgcctc cacaccgct tcaaccagac ggccacggcc 2160
acgggcaggc taagtagctc cgatcccaac ctccagaaca tcccgtccg caccctgctt 2220
gggcagagga tccgccgggc ctcatcgcc gaggaggggt ggctattggg ggccatggac 2280
tatagccaga tagagctcag ggtgctggcc cactctccg gcgacgagaa cctgatccgg 2340
gtcttccagg aggggcggga catccacacg gagaccgcca gctggatgtt cggcgtcccc 2400
cgggaggccg tggaccccc gatgcgccgg gcggccaaga ccatcaactt cggggctcctc 2460
tacggcatgt cggcccaccg cctctcccag gagctagcca tcccttacga ggaggcccag 2520
gccttcattg agcgctactt tcagagcttc cccaagggtg gggcctggat tgagaagacc 2580
ctggaggagg gcaggaggcg ggggtacgtg gagaccctct tcggccggcg ccgctactgt 2640
ccagacctag agggccgggt gaagagcgtg cgggaggcgg ccgagcgcat ggccttcaac 2700
atgcccgtcc agggcaccgc cgccgacctc atgaagctgg ctatggtgaa gctcttcccc 2760
aggctggagg aaatgggggc caggatgctc cttcagggtc acgacgagct ggtcctcgag 2820
gccccaaaag agagggcgga ggccgtggcc cggctggcca aggaggtcat ggaggggggtg 2880
tatcccctgg ccgtgcccct ggaggtggag gtggggatag gggaggactg gctctccgcc 2940
aaggagtga

```

<210> 7

<211> 910

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: poly amino acids

<400> 7

```

Met Arg Gly Ser His His His His His His Ala Ala Asp Asp Asp Asp
1           5           10           15

```

Lys Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
                     20                    25                    30  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
                     35                    40                    45  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
                     50                    55                    60  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
                     65                    70                    75                    80  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
                     85                    90                    95  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
                     100                    105                    110  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
                     115                    120                    125  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
                     130                    135                    140  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
                     145                    150                    155                    160  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
                     165                    170                    175  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
                     180                    185                    190  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
                     195                    200                    205  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
                     210                    215                    220  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
                     225                    230                    235                    240  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
                     245                    250                    255  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
                     260                    265                    270  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
                     275                    280                    285  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
                     290                    295                    300  
 Leu Glu Ser Pro Tyr Asp Asn Tyr Val Thr Ile Leu Asp Glu Glu Thr  
                     305                    310                    315                    320  
 Leu Lys Ala Trp Ile Ala Lys Leu Glu Lys Ala Pro Val Phe Ala Phe  
                     325                    330                    335  
 Asp Thr Glu Thr Asp Ser Leu Asp Asn Ile Ser Ala Asn Leu Val Gly  
                     340                    345                    350

Leu Ser Phe Ala Ile Glu Pro Gly Val Ala Ala Tyr Ile Pro Val Ala  
 355 360 365  
 His Asp Tyr Leu Asp Ala Pro Asp Gln Ile Ser Arg Glu Arg Ala Leu  
 370 375 380  
 Glu Leu Leu Lys Pro Leu Leu Glu Asp Glu Lys Ala Leu Lys Val Gly  
 385 390 395 400  
 Gln Asn Leu Lys Tyr Asp Arg Gly Ile Leu Ala Asn Tyr Gly Ile Glu  
 405 410 415  
 Leu Arg Gly Ile Ala Phe Asp Thr Met Leu Glu Ser Tyr Ile Leu Asn  
 420 425 430  
 Ser Val Ala Gly Arg His Asp Met Asp Ser Leu Ala Glu Arg Trp Leu  
 435 440 445  
 Lys His Lys Thr Ile Thr Phe Glu Glu Ile Ala Gly Lys Gly Lys Asn  
 450 455 460  
 Gln Leu Thr Phe Asn Gln Ile Ala Leu Glu Glu Ala Gly Arg Tyr Ala  
 465 470 475 480  
 Ala Glu Asp Ala Asp Val Thr Leu Gln Leu His Leu Lys Met Trp Pro  
 485 490 495  
 Asp Leu Gln Lys His Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu  
 500 505 510  
 Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg  
 515 520 525  
 Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu  
 530 535 540  
 Val Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe  
 545 550 555 560  
 Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu  
 565 570 575  
 Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr  
 580 585 590  
 Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu  
 595 600 605  
 Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile  
 610 615 620  
 Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr  
 625 630 635 640  
 Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 645 650 655  
 Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile  
 660 665 670  
 Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp  
 675 680 685



Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu  
 690 695 700  
 Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr  
 705 710 715 720  
 Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met  
 725 730 735  
 Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser  
 740 745 750  
 Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln  
 755 760 765  
 Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp  
 770 775 780  
 Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr  
 785 790 795 800  
 Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys  
 805 810 815  
 Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln  
 820 825 830  
 Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro  
 835 840 845  
 Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu  
 850 855 860  
 Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu  
 865 870 875 880  
 Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu  
 885 890 895  
 Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 900 905 910

<210> 8  
 <211> 910  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: poly amino  
 acids

<400> 8  
 Met Arg Gly Ser His His His His His Ala Ala Asp Asp Asp Asp  
 1 5 10 15  
 Lys Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 20 25 30  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 35 40 45

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 50 55 60  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 65 70 75 80  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 85 90 95  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 100 105 110  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 115 120 125  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 130 135 140  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 145 150 155 160  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 165 170 175  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 180 185 190  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 195 200 205  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 210 215 220  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 225 230 235 240  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 245 250 255  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 260 265 270  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 275 280 285  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 290 295 300  
 Leu Glu Ser Pro Tyr Asp Asn Tyr Val Thr Ile Leu Asp Glu Glu Thr  
 305 310 315 320  
 Leu Lys Ala Trp Ile Ala Lys Leu Glu Lys Ala Pro Val Phe Ala Phe  
 325 330 335  
 Asp Thr Glu Thr Asp Ser Leu Asp Asn Ile Ser Ala Asn Leu Val Gly  
 340 345 350  
 Leu Ser Phe Ala Ile Glu Pro Gly Val Ala Ala Tyr Ile Pro Val Ala  
 355 360 365  
 His Asp Tyr Leu Asp Ala Pro Asp Gln Ile Ser Arg Glu Arg Ala Leu  
 370 375 380

Glu Leu Leu Lys Pro Leu Leu Glu Asp Glu Lys Ala Leu Lys Val Gly  
 385 390 395 400  
 Gln Asn Leu Lys Tyr Asp Arg Gly Ile Leu Ala Asn Tyr Gly Ile Glu  
 405 410 415  
 Leu Arg Gly Ile Ala Phe Asp Thr Met Leu Glu Ser Tyr Ile Leu Asn  
 420 425 430  
 Ser Val Ala Gly Arg His Asp Met Asp Ser Leu Ala Glu Arg Trp Leu  
 435 440 445  
 Lys His Lys Thr Ile Thr Phe Glu Glu Ile Ala Gly Lys Gly Lys Asn  
 450 455 460  
 Gln Leu Thr Phe Asn Gln Ile Ala Leu Glu Glu Ala Gly Arg Tyr Ala  
 465 470 475 480  
 Ala Glu Asp Ala Asp Val Thr Leu Gln Leu His Leu Lys Met Trp Pro  
 485 490 495  
 Asp Leu Gln Lys His Lys Gly Pro Leu Asn Val Phe Glu Asn Ile Glu  
 500 505 510  
 Met Pro Leu Val Pro Val Leu Ser Arg Ile Glu Arg Asn Gly Val Arg  
 515 520 525  
 Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu  
 530 535 540  
 Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe  
 545 550 555 560  
 Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu  
 565 570 575  
 Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr  
 580 585 590  
 Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu  
 595 600 605  
 Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile  
 610 615 620  
 Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr  
 625 630 635 640  
 Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 645 650 655  
 Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile  
 660 665 670  
 Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp  
 675 680 685  
 Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu  
 690 695 700  
 Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr  
 705 710 715 720

Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met  
725 730 735

Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser  
740 745 750

Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln  
755 760 765

Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp  
770 775 780

Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr  
785 790 795 800

Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys  
805 810 815

Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln  
820 825 830

Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro  
835 840 845

Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu  
850 855 860

Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu  
865 870 875 880

Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu  
885 890 895

Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
900 905 910

<210> 9

<211> 908

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: poly amino  
acids

<400> 9

Met Arg Gly Ser His His His His His His Ala Ala Asp Asp Asp Asp  
1 5 10 15

Lys Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
20 25 30

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
35 40 45

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
50 55 60

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
65 70 75 80

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
85 90 95  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
100 105 110  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
115 120 125  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
130 135 140  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
145 150 155 160  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
165 170 175  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
180 185 190  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
195 200 205  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
210 215 220  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
225 230 235 240  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
245 250 255  
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
260 265 270  
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
275 280 285  
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
290 295 300  
Leu Glu Ser Pro Pro Val Gly Tyr Arg Ile Val Lys Asp Leu Val Glu  
305 310 315 320  
Phe Glu Lys Leu Ile Glu Lys Leu Arg Glu Ser Pro Ser Phe Ala Ile  
325 330 335  
Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asp Cys Asp Ile Val Gly  
340 345 350  
Ile Ser Val Ser Phe Lys Pro Lys Glu Ala Tyr Tyr Ile Pro Leu His  
355 360 365  
His Arg Asn Ala Gln Asn Leu Asp Glu Lys Glu Val Leu Lys Lys Leu  
370 375 380  
Lys Glu Ile Leu Glu Asp Pro Gly Ala Lys Ile Val Gly Gln Asn Leu  
385 390 395 400  
Lys Phe Asp Tyr Lys Val Leu Met Val Lys Gly Val Glu Pro Val Pro  
405 410 415

Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro Asn Glu  
 420 425 430  
 Lys Lys Phe Asn Leu Asp Asp Leu Ala Leu Lys Phe Leu Gly Tyr Lys  
 435 440 445  
 Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu Phe Gly  
 450 455 460  
 Phe Ser Phe Ala Asp Val Pro Val Glu Lys Ala Ala Asn Tyr Ser Cys  
 465 470 475 480  
 Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser Leu Lys  
 485 490 495  
 Leu His Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro  
 500 505 510  
 Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp  
 515 520 525  
 Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala  
 530 535 540  
 Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu  
 545 550 555 560  
 Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu  
 565 570 575  
 Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala  
 580 585 590  
 Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile  
 595 600 605  
 Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro  
 610 615 620  
 Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe  
 625 630 635 640  
 Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn  
 645 650 655  
 Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg  
 660 665 670  
 Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser  
 675 680 685  
 Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu  
 690 695 700  
 Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser  
 705 710 715 720  
 Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg  
 725 730 735  
 Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His  
 740 745 750

Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe  
           755                                  760                                  765  
 Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu  
           770                                  775                                  780  
 Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe  
           785                                  790                                  795                                  800  
 Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val  
                                   805                                  810                                  815  
 Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr  
                                   820                                  825                                  830  
 Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu  
                                   835                                  840                                  845  
 Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val  
           850                                  855                                  860  
 Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys  
           865                                  870                                  875                                  880  
 Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu  
                                   885                                  890                                  895  
 Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
                                   900                                  905

<210> 10  
 <211> 908  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: poly amino  
           acids

<400> 10  
 Met Arg Gly Ser His His His His His His Ala Ala Asp Asp Asp Asp  
       1                                  5                                  10                                  15  
 Lys Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
           20                                  25                                  30  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
           35                                  40                                  45  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
           50                                  55                                  60  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
           65                                  70                                  75                                  80  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
                                   85                                  90                                  95  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
                                   100                                  105                                  110

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 115 120 125  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 130 135 140  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 145 150 155 160  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 165 170 175  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 180 185 190  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 195 200 205  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 210 215 220  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 225 230 235 240  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 245 250 255  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 260 265 270  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 275 280 285  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 290 295 300  
 Leu Glu Ser Pro Pro Val Gly Tyr Arg Ile Val Lys Asp Leu Val Glu  
 305 310 315 320  
 Phe Glu Lys Leu Ile Glu Lys Leu Arg Glu Ser Pro Ser Phe Ala Ile  
 325 330 335  
 Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asp Cys Asp Ile Val Gly  
 340 345 350  
 Ile Ser Val Ser Phe Lys Pro Lys Glu Ala Tyr Tyr Ile Pro Leu His  
 355 360 365  
 His Arg Asn Ala Gln Asn Leu Asp Glu Lys Glu Val Leu Lys Lys Leu  
 370 375 380  
 Lys Glu Ile Leu Glu Asp Pro Gly Ala Lys Ile Val Gly Gln Asn Leu  
 385 390 395 400  
 Lys Phe Asp Tyr Lys Val Leu Met Val Lys Gly Val Glu Pro Val Pro  
 405 410 415  
 Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro Asn Glu  
 420 425 430  
 Lys Lys Phe Asn Leu Asp Asp Leu Ala Leu Lys Phe Leu Gly Tyr Lys  
 435 440 445



Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu Phe Gly  
 450 455 460  
 Phe Ser Phe Ala Asp Val Pro Val Glu Lys Ala Ala Asn Tyr Ser Cys  
 465 470 475 480  
 Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser Leu Lys  
 485 490 495  
 Leu His Glu Ala Asp Leu Glu Asn Val Phe Tyr Lys Ile Glu Met Pro  
 500 505 510  
 Leu Val Ser Val Leu Ala Arg Met Glu Leu Asn Gly Val Arg Leu Asp  
 515 520 525  
 Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala  
 530 535 540  
 Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu  
 545 550 555 560  
 Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu  
 565 570 575  
 Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala  
 580 585 590  
 Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile  
 595 600 605  
 Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro  
 610 615 620  
 Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe  
 625 630 635 640  
 Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn  
 645 650 655  
 Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg  
 660 665 670  
 Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser  
 675 680 685  
 Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu  
 690 695 700  
 Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser  
 705 710 715 720  
 Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg  
 725 730 735  
 Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His  
 740 745 750  
 Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe  
 755 760 765  
 Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu  
 770 775 780

Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe  
 785 790 795 800  
 Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val  
 805 810 815  
 Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr  
 820 825 830  
 Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu  
 835 840 845  
 Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val  
 850 855 860  
 Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys  
 865 870 875 880  
 Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu  
 885 890 895  
 Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu  
 900 905

<210> 11  
 <211> 949  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: poly amino  
 acids

<400> 11  
 Met Arg Gly Ser His His His His His Ala Ala Asp Asp Asp Asp  
 1 5 10 15  
 Lys Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
 20 25 30  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
 35 40 45  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
 50 55 60  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 65 70 75 80  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 85 90 95  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 100 105 110  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
 115 120 125  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 130 135 140

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 145 150 155 160  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 165 170 175  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 180 185 190  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 195 200 205  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 210 215 220  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 225 230 235 240  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 245 250 255  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 260 265 270  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 275 280 285  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 290 295 300  
 Leu Glu Ser Pro His Pro Ala Val Val Asp Ile Phe Glu Tyr Asp Ile  
 305 310 315 320  
 Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro Met Glu  
 325 330 335  
 Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr Leu Tyr  
 340 345 350  
 His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile Ser Tyr  
 355 360 365  
 Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile Asp Leu  
 370 375 380  
 Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys Arg Phe  
 385 390 395 400  
 Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr Tyr Asn  
 405 410 415  
 Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu Lys Leu  
 420 425 430  
 Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys Met Gln  
 435 440 445  
 Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile His Phe  
 450 455 460  
 Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr Tyr Thr  
 465 470 475 480

Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu Lys Val  
 485 490 495  
 Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn Leu Glu  
 500 505 510  
 Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr Glu Leu  
 515 520 525  
 Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Glu Arg Leu Leu  
 530 535 540  
 Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His  
 545 550 555 560  
 Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu  
 565 570 575  
 Ser Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe  
 580 585 590  
 Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu  
 595 600 605  
 Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu  
 610 615 620  
 Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg  
 625 630 635 640  
 Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr  
 645 650 655  
 Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro  
 660 665 670  
 Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr  
 675 680 685  
 Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg  
 690 695 700  
 Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly  
 705 710 715 720  
 Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu  
 725 730 735  
 Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly  
 740 745 750  
 Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg  
 755 760 765  
 Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe  
 770 775 780  
 Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala  
 785 790 795 800  
 Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser  
 805 810 815

Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg  
                   820                  825                  830  
 Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro  
                   835                  840                  845  
 Asp Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met  
                   850                  855                  860  
 Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu  
                   865                  870                  875                  880  
 Ala Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met  
                   885                  890                  895  
 Leu Leu Gln Val His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg  
                   900                  905                  910  
 Ala Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr  
                   915                  920                  925  
 Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp  
                   930                  935                  940  
 Leu Ser Ala Lys Glu  
 945

<210> 12  
 <211> 982  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: poly amino  
           acids

<400> 12  
 Met Arg Gly Ser His His His His His His Ala Ala Asp Asp Asp Asp  
   1                  5                  10                  15  
 Lys Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu  
                   20                  25                  30  
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys  
                   35                  40                  45  
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
                   50                  55                  60  
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
                   65                  70                  75                  80  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
                   85                  90                  95  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
                   100                  105                  110  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu  
                   115                  120                  125

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 130 135 140  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 145 150 155 160  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 165 170 175  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 180 185 190  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 195 200 205  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 210 215 220  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 225 230 235 240  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 245 250 255  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 260 265 270  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 275 280 285  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 290 295 300  
 Leu Glu Ser Pro Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu  
 305 310 315 320  
 Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile  
 325 330 335  
 Pro Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu  
 340 345 350  
 Thr Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met  
 355 360 365  
 Ile Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn  
 370 375 380  
 Ile Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile  
 385 390 395 400  
 Lys Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val  
 405 410 415  
 Thr Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala  
 420 425 430  
 Glu Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro  
 435 440 445  
 Lys Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg  
 450 455 460

Ile His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro  
 465 470 475 480  
 Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys  
 485 490 495  
 Glu Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu  
 500 505 510  
 Asn Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr  
 515 520 525  
 Tyr Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg  
 530 535 540  
 Leu Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn  
 545 550 555 560  
 Leu Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val  
 565 570 575  
 Ala Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu  
 580 585 590  
 Ser Tyr Thr Gly Gly Phe Val Arg Leu Asp Val Ala Tyr Leu Arg Ala  
 595 600 605  
 Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val  
 610 615 620  
 Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu  
 625 630 635 640  
 Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr  
 645 650 655  
 Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu  
 660 665 670  
 Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu  
 675 680 685  
 Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His  
 690 695 700  
 Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala  
 705 710 715 720  
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val  
 725 730 735  
 Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu  
 740 745 750  
 Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val  
 755 760 765  
 Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu  
 770 775 780  
 Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro  
 785 790 795 800





<210> 15  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide

<400> 15  
 gaggcctacg ggcatcacca tcaccatcac ggggtacaagg cg

42

<210> 16  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: polypeptide

<400> 16  
 Glu Ala Tyr Gly His His His His His Gly Tyr Lys Ala  
           1                  5                  10

<210> 17  
 <211> 894  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: amino acid

<400> 17  
 Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala  
           1                  5                  10                  15  
 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
                   20                  25                  30  
 Asn Ala Thr Tyr Gly Val Ala Arg Met Leu Val Arg Phe Ile Lys Asp  
           35                  40                  45  
 His Ile Ile Val Gly Lys Asp Tyr Val Ala Val Ala Phe Asp Lys Lys  
           50                  55                  60  
 Ala Ala Thr Phe Arg His Lys Leu Leu Glu Thr Tyr Lys Ala Gln Arg  
           65                  70                  75                  80  
 Pro Lys Thr Pro Asp Leu Leu Ile Gln Gln Leu Pro Tyr Ile Lys Lys  
                   85                  90                  95  
 Leu Val Glu Ala Leu Gly Met Lys Val Leu Glu Val Glu Gly Tyr Glu  
                   100                  105                  110  
 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Leu Pro Leu Phe  
           115                  120                  125  
 Asp Glu Ile Phe Ile Val Thr Gly Asp Lys Asp Met Leu Gln Leu Val

130					135					140					
Asn	Glu	Lys	Ile	Lys	Val	Trp	Arg	Ile	Val	Lys	Gly	Ile	Ser	Asp	Leu
145					150					155					160
Glu	Leu	Tyr	Asp	Ala	Gln	Lys	Val	Lys	Glu	Lys	Tyr	Gly	Val	Glu	Pro
				165					170					175	
Gln	Gln	Ile	Pro	Asp	Leu	Leu	Ala	Leu	Thr	Gly	Asp	Glu	Ile	Asp	Asn
			180					185					190		
Ile	Pro	Gly	Val	Thr	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Gln	Leu	Leu
		195					200					205			
Glu	Lys	Tyr	Lys	Asp	Leu	Glu	Asp	Ile	Leu	Asn	His	Val	Arg	Glu	Leu
	210					215					220				
Pro	Gln	Lys	Val	Arg	Lys	Ala	Leu	Leu	Arg	Asp	Arg	Glu	Asn	Ala	Ile
225					230					235					240
Leu	Ser	Lys	Lys	Leu	Ala	Ile	Leu	Glu	Thr	Asn	Val	Pro	Ile	Glu	Ile
				245					250					255	
Asn	Trp	Glu	Glu	Leu	Arg	Tyr	Gln	Gly	Tyr	Asp	Arg	Glu	Lys	Leu	Leu
			260					265					270		
Pro	Leu	Leu	Lys	Glu	Leu	Glu	Phe	Ala	Ser	Ile	Met	Lys	Glu	Leu	Gln
		275					280					285			
Leu	Tyr	Glu	Glu	Ser	Glu	Pro	Val	Gly	Tyr	Arg	Ile	Val	Lys	Asp	Leu
	290					295					300				
Val	Glu	Phe	Glu	Lys	Leu	Ile	Glu	Lys	Leu	Arg	Glu	Ser	Pro	Ser	Phe
305					310					315					320
Ala	Ile	Asp	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asp	Cys	Asp	Ile
				325					330					335	
Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Glu	Ala	Tyr	Tyr	Ile	Pro
			340					345					350		
Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	Lys	Glu	Val	Leu	Lys
		355					360					365			
Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Gly	Ala	Lys	Ile	Val	Gly	Gln
	370					375					380				
Asn	Leu	Lys	Phe	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Val	Glu	Pro
385					390					395					400
Val	Pro	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro
				405					410					415	
Asn	Glu	Lys	Lys	Phe	Asn	Leu	Asp	Asp	Leu	Ala	Leu	Lys	Phe	Leu	Gly
			420					425					430		
Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Ser	Pro	Leu
		435					440					445			
Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Glu	Lys	Ala	Ala	Asn	Tyr
	450					455					460				

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser  
 465 470 475 480  
 Leu Lys Leu His Glu Ala Asp Leu Glu Asn Val Phe Tyr Lys Ile Glu  
 485 490 495  
 Met Pro Leu Val Ser Val Leu Ala Arg Met Glu Leu Asn Gly Val Lys  
 500 505 510  
 Val Asp Arg Asp Ala Leu Ile Gln Tyr Thr Lys Glu Ile Glu Asn Lys  
 515 520 525  
 Ile Leu Lys Leu Glu Thr Gln Ile Tyr Gln Ile Ala Gly Glu Trp Phe  
 530 535 540  
 Asn Ile Asn Ser Pro Lys Gln Leu Ser Tyr Ile Leu Phe Glu Lys Leu  
 545 550 555 560  
 Lys Leu Pro Val Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Asp Ala  
 565 570 575  
 Glu Val Leu Glu Glu Leu Phe Asp Lys His Glu Ile Val Pro Leu Ile  
 580 585 590  
 Leu Asp Tyr Arg Met Tyr Thr Lys Ile Leu Thr Thr Tyr Cys Gln Gly  
 595 600 605  
 Leu Leu Gln Ala Ile Asn Pro Ser Ser Gly Arg Val His Thr Thr Phe  
 610 615 620  
 Ile Gln Thr Gly Thr Ala Thr Gly Arg Leu Ala Ser Ser Asp Pro Asn  
 625 630 635 640  
 Leu Gln Asn Ile Pro Val Lys Tyr Asp Glu Gly Lys Leu Ile Arg Lys  
 645 650 655  
 Val Phe Val Pro Glu Gly Gly His Val Leu Ile Asp Ala Asp Tyr Ser  
 660 665 670  
 Gln Ile Glu Leu Arg Ile Leu Ala His Ile Ser Glu Asp Glu Arg Leu  
 675 680 685  
 Ile Ser Ala Phe Lys Asn Asn Val Asp Ile His Ser Gln Thr Ala Ala  
 690 695 700  
 Glu Val Phe Gly Val Asp Ile Ala Asp Val Thr Pro Glu Met Arg Ser  
 705 710 715 720  
 Gln Ala Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr  
 725 730 735  
 Gly Leu Ala Arg Asp Ile Lys Ile Ser Arg Lys Glu Ala Ala Glu Phe  
 740 745 750  
 Ile Asn Lys Tyr Phe Glu Arg Tyr Pro Lys Val Lys Glu Tyr Leu Asp  
 755 760 765  
 Asn Thr Val Lys Phe Ala Arg Asp Asn Gly Phe Val Leu Thr Leu Phe  
 770 775 780  
 Asn Arg Lys Arg Tyr Ile Lys Asp Ile Lys Ser Thr Asn Arg Asn Leu  
 785 790 795 800

Arg Gly Tyr Ala Glu Arg Ile Ala Met Asn Ser Pro Ile Gln Gly Ser  
 805 810 815  
 Ala Ala Asp Ile Met Lys Leu Ala Met Ile Lys Val Tyr Gln Lys Leu  
 820 825 830  
 Lys Glu Asn Asn Leu Lys Ser Lys Ile Ile Leu Gln Val His Asp Glu  
 835 840 845  
 Leu Leu Ile Glu Ala Pro Tyr Glu Glu Lys Asp Ile Val Lys Glu Ile  
 850 855 860  
 Val Lys Arg Glu Met Glu Asn Ala Val Ala Leu Lys Val Pro Leu Val  
 865 870 875 880  
 Val Glu Val Lys Glu Gly Leu Asn Trp Tyr Glu Asn Lys Ile  
 885 890

<210> 18  
 <211> 893  
 <212> PRT  
 <213> T. neapolitana

<400> 18  
 Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala  
 1 5 10 15  
 Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr  
 20 25 30  
 Asn Ala Thr Tyr Gly Val Ala Arg Met Leu Val Arg Phe Ile Lys Asp  
 35 40 45  
 His Ile Ile Val Gly Lys Asp Tyr Val Ala Val Ala Phe Asp Lys Lys  
 50 55 60  
 Ala Ala Thr Phe Arg His Lys Leu Leu Glu Thr Tyr Lys Ala Gln Arg  
 65 70 75 80  
 Pro Lys Thr Pro Asp Leu Leu Ile Gln Gln Leu Pro Tyr Ile Lys Lys  
 85 90 95  
 Leu Val Glu Ala Leu Gly Met Lys Val Leu Glu Val Glu Gly Tyr Glu  
 100 105 110  
 Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Lys Gly Leu Pro Leu Phe  
 115 120 125  
 Asp Glu Ile Phe Ile Val Thr Gly Asp Lys Asp Met Leu Gln Leu Val  
 130 135 140  
 Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu  
 145 150 155 160  
 Glu Leu Tyr Asp Ala Gln Lys Val Lys Glu Lys Tyr Gly Val Glu Pro  
 165 170 175  
 Gln Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Glu Ile Asp Asn  
 180 185 190  
 Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu

195					200					205					
Glu	Lys	Tyr	Lys	Asp	Leu	Glu	Asp	Ile	Leu	Asn	His	Val	Arg	Glu	Leu
210						215					220				
Pro	Gln	Lys	Val	Arg	Lys	Ala	Leu	Leu	Arg	Asp	Arg	Glu	Asn	Ala	Ile
225					230					235					240
Leu	Ser	Lys	Lys	Leu	Ala	Ile	Leu	Glu	Thr	Asn	Val	Pro	Ile	Glu	Ile
				245					250					255	
Asn	Trp	Glu	Glu	Leu	Arg	Tyr	Gln	Gly	Tyr	Asp	Arg	Glu	Lys	Leu	Leu
			260					265					270		
Pro	Leu	Leu	Lys	Glu	Leu	Glu	Phe	Ala	Ser	Ile	Met	Lys	Glu	Leu	Gln
		275					280					285			
Leu	Tyr	Glu	Glu	Ser	Glu	Pro	Val	Gly	Tyr	Arg	Ile	Val	Lys	Asp	Leu
290						295					300				
Val	Glu	Phe	Glu	Lys	Leu	Ile	Glu	Lys	Leu	Arg	Glu	Ser	Pro	Ser	Phe
305					310					315					320
Ala	Ile	Asp	Leu	Glu	Thr	Ser	Ser	Leu	Asp	Pro	Phe	Asp	Cys	Asp	Ile
				325					330					335	
Val	Gly	Ile	Ser	Val	Ser	Phe	Lys	Pro	Lys	Glu	Ala	Tyr	Tyr	Ile	Pro
			340					345					350		
Leu	His	His	Arg	Asn	Ala	Gln	Asn	Leu	Asp	Glu	Lys	Glu	Val	Leu	Lys
		355					360					365			
Lys	Leu	Lys	Glu	Ile	Leu	Glu	Asp	Pro	Gly	Ala	Lys	Ile	Val	Gly	Gln
	370					375					380				
Asn	Leu	Lys	Phe	Asp	Tyr	Lys	Val	Leu	Met	Val	Lys	Gly	Val	Glu	Pro
385				390						395					400
Val	Pro	Pro	His	Phe	Asp	Thr	Met	Ile	Ala	Ala	Tyr	Leu	Leu	Glu	Pro
			405						410					415	
Asn	Glu	Lys	Lys	Phe	Asn	Leu	Asp	Asp	Leu	Ala	Leu	Lys	Phe	Leu	Gly
			420					425					430		
Tyr	Lys	Met	Thr	Ser	Tyr	Gln	Glu	Leu	Met	Ser	Phe	Ser	Ser	Pro	Leu
		435					440					445			
Phe	Gly	Phe	Ser	Phe	Ala	Asp	Val	Pro	Val	Glu	Lys	Ala	Ala	Asn	Tyr
	450					455					460				
Ser	Cys	Glu	Asp	Ala	Asp	Ile	Thr	Tyr	Arg	Leu	Tyr	Lys	Ile	Leu	Ser
465					470					475					480
Leu	Lys	Leu	His	Glu	Ala	Asp	Leu	Glu	Asn	Val	Phe	Tyr	Lys	Ile	Glu
				485					490					495	
Met	Pro	Leu	Val	Ser	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly	Val	Tyr
			500					505					510		
Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly	Lys	Lys
		515					520					525			

Leu Glu Glu Leu Ala Glu Glu Ile Tyr Arg Ile Ala Gly Glu Pro Phe  
 530 535 540  
 Asn Ile Asn Ser Pro Lys Gln Val Ser Arg Ile Leu Phe Glu Lys Leu  
 545 550 555 560  
 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Asp Tyr Ser Thr  
 565 570 575  
 Arg Ile Glu Val Leu Glu Glu Leu Ala Gly Glu His Glu Ile Ile Pro  
 580 585 590  
 Leu Ile Leu Glu Tyr Arg Lys Ile Gln Lys Leu Lys Ser Thr Tyr Ile  
 595 600 605  
 Asp Ala Leu Pro Lys Met Val Asn Pro Lys Thr Gly Arg Ile His Ala  
 610 615 620  
 Ser Phe Asn Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp  
 625 630 635 640  
 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile  
 645 650 655  
 Arg Lys Ala Ile Val Pro Gln Asp Pro Asn Trp Trp Ile Val Ser Ala  
 660 665 670  
 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp  
 675 680 685  
 Glu Asn Leu Leu Arg Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu  
 690 695 700  
 Thr Ala Ser Arg Ile Phe Asn Val Lys Pro Glu Glu Val Thr Glu Glu  
 705 710 715 720  
 Met Arg Arg Ala Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val  
 725 730 735  
 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Val Pro Val Lys Glu Ala  
 740 745 750  
 Glu Lys Met Ile Val Asn Tyr Phe Val Leu Tyr Pro Lys Val Arg Asp  
 755 760 765  
 Tyr Ile Gln Arg Val Val Ser Glu Ala Lys Glu Lys Gly Tyr Val Arg  
 770 775 780  
 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp  
 785 790 795 800  
 Arg Asn Thr Gln Ala Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile  
 805 810 815  
 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Glu Ile Asp  
 820 825 830  
 Arg Glu Leu Lys Glu Arg Lys Met Arg Ser Lys Met Ile Ile Gln Val  
 835 840 845  
 His Asp Glu Leu Val Phe Glu Val Pro Asn Glu Glu Lys Asp Ala Leu  
 850 855 860

Val Glu Leu Val Lys Asp Arg Met Thr Asn Val Val Lys Leu Ser Val  
 865 870 875 880

Pro Leu Glu Val Asp Val Thr Ile Gly Lys Thr Trp Ser  
 885 890

<210> 19  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 19  
 ctgaccatgg cgagactatt tctctttg 28

<210> 20  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 20  
 tctgtcgcacc ttcacaccgt tcagttccat cc 32

<210> 21  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 21  
 aaggtcgaca gagatgccct catccaatat acc 33

<210> 22  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 22  
 tagcaagctt ctattttgtc tcataaccagt 30

<210> 23  
 <211> 60  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: polypeptide

<400> 23  
 Ile Glu Met Pro Leu Val Ser Val Leu Ala Arg Met Glu Leu Asn Gly

1	5	10	15
Val Lys Val Asp Arg Asp Ala Leu Ile Gln Tyr Thr Lys Glu Ile Glu	20	25	30
Asn Lys Ile Leu Lys Leu Glu Thr Gln Ile Tyr Gln Ile Ala Gly Glu	35	40	45
Trp Phe Asn Ile Asn Ser Pro Lys Gln Leu Ser Tyr	50	55	60

<210> 24  
 <211> 60  
 <212> PRT  
 <213> T. neapolitana

<400> 24
Ile Glu Met Pro Leu Val Ser Val Leu Ala Arg Met Glu Leu Asn Gly
1 5 10 15
Val Tyr Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly
20 25 30
Lys Lys Leu Glu Glu Leu Ala Glu Glu Ile Tyr Arg Ile Ala Gly Glu
35 40 45
Pro Phe Asn Ile Asn Ser Pro Lys Gln Val Ser Arg
50 55 60

<210> 25  
 <211> 60  
 <212> PRT  
 <213> Anaerocellum thermophilum

<400> 25
Ile Glu Arg Pro Leu Ile Pro Val Leu Tyr Glu Met Glu Lys Thr Gly
1 5 10 15
Phe Lys Val Asp Arg Asp Ala Leu Ile Gln Tyr Thr Lys Glu Ile Glu
20 25 30
Asn Lys Ile Leu Lys Leu Glu Thr Gln Ile Tyr Gln Ile Ala Gly Glu
35 40 45
Trp Phe Asn Ile Asn Ser Pro Lys Gln Leu Ser Tyr
50 55 60

<210> 26  
 <211> 27  
 <212> DNA  
 <213> T. neapolitana

<400> 26  
 atggcgagac tatttctctt tgatgga

27

<210> 27  
 <211> 9  
 <212> PRT  
 <213> T. neapolitana



<400> 27  
Met Ala Arg Leu Phe Leu Phe Asp Gly  
1 5

<210> 28  
<211> 51  
<212> DNA  
<213> T. neapolitana

<400> 28  
cggatggaac tgaacggtgt gtacgtggac acagagttcc tgaagaaact c 51

<210> 29  
<211> 17  
<212> PRT  
<213> T. neapolitana

<400> 29  
Arg Met Glu Leu Asn Gly Val Tyr Val Asp Thr Glu Phe Leu Lys Lys  
1 5 10 15

Leu

<210> 30  
<211> 51  
<212> DNA  
<213> Anaerocellum thermophilum

<400> 30  
atggaaaaaa caggatttaa ggtggataga gatgccctca tccaatatac c 51

<210> 31  
<211> 17  
<212> PRT  
<213> Anaerocellum thermophilum

<400> 31  
Met Glu Lys Thr Gly Phe Lys Val Asp Arg Asp Ala Leu Ile Gln Tyr  
1 5 10 15

Thr

<210> 32  
<211> 27  
<212> DNA  
<213> Anaerocellum thermophilum

<400> 32  
ggactgaact ggtatgagac aaaatag 27

<210> 33  
<211> 8  
<212> PRT  
<213> Anaerocellum thermophilum

<400> 33  
Gly Leu Asn Trp Tyr Glu Thr Lys

1

5

&lt;210&gt; 34

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: amino acid

&lt;400&gt; 34

Ile	Met	Glu	Pro	Leu	Val	Ser	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly
1				5					10					15	

Val	Tyr	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly
			20					25					30		

Lys	Lys	Leu	Glu	Glu	Leu	Ala	Glu	Glu	Ile	Tyr	Arg	Ile	Ala	Gly	Glu
		35					40					45			

Pro	Phe	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Arg
	50					55					60

&lt;210&gt; 35

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; T. neapolitana

&lt;400&gt; 35

Ile	Glu	Met	Pro	Leu	Val	Ser	Val	Leu	Ala	Arg	Met	Glu	Leu	Asn	Gly
1				5					10					15	

Val	Tyr	Val	Asp	Thr	Glu	Phe	Leu	Lys	Lys	Leu	Ser	Glu	Glu	Tyr	Gly
			20					25					30		

Lys	Lys	Leu	Glu	Glu	Leu	Ala	Glu	Glu	Ile	Tyr	Arg	Ile	Ala	Gly	Glu
		35					40					45			

Pro	Phe	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Val	Ser	Arg
	50					55					60

&lt;210&gt; 36

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Anaerocellum thermophilum

&lt;400&gt; 36

Ile	Glu	Arg	Pro	Leu	Ile	Pro	Val	Leu	Tyr	Glu	Met	Glu	Lys	Thr	Gly
1				5					10					15	

Phe	Lys	Val	Asp	Arg	Asp	Ala	Leu	Ile	Gln	Tyr	Thr	Lys	Glu	Ile	Glu
			20					25					30		

Asn	Lys	Ile	Leu	Lys	Leu	Glu	Thr	Gln	Ile	Tyr	Gln	Ile	Ala	Gly	Glu
		35					40					45			

Trp	Phe	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Leu	Ser	Arg
	50					55					60

<210> 37  
 <211> 48  
 <212> DNA  
 <213> T. neapolitana  
  
 <400> 37  
 tcaccgaagc aggtttcaag gatccttttt gaaaaactcg gcataaaa 48  
  
 <210> 38  
 <211> 16  
 <212> PRT  
 <213> T. neapolitana  
  
 <400> 38  
 Ser Pro Lys Gln Val Ser Arg Ile Leu Phe Glu Lys Leu Gly Ile Lys  
 1 5 10 15  
  
 <210> 39  
 <211> 48  
 <212> DNA  
 <213> Anaerocellum thermophilum  
  
 <400> 39  
 tcaccgaaac agctttctta cattttgttt gaaaagctaa aacttcct 48  
  
 <210> 40  
 <211> 16  
 <212> PRT  
 <213> Anaerocellum thermophilum  
  
 <400> 40  
 Ser Pro Lys Gln Leu Ser Tyr Ile Leu Phe Glu Lys Leu Lys Leu Pro  
 1 5 10 15  
  
 <210> 41  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: amino acid  
  
 <400> 41  
 caccgaaaca gctttctagg atcctgtttg aaaagctaaa acttcct 47  
  
 <210> 42  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: amino acid  
  
 <400> 42  
 gtggctttgt cgaaagatcc taggacaaac ttttcgattt tgaaggac 48  
  
 <210> 43

<211> 851  
 <212> PRT  
 <213> Anaerocellum thermophilum

<400> 43

Met	Lys	Leu	Val	Ile	Phe	Asp	Gly	Asn	Ser	Ile	Leu	Tyr	Arg	Ala	Phe
1				5					10					15	
Phe	Ala	Leu	Pro	Glu	Leu	Thr	Thr	Ser	Asn	Asn	Ile	Pro	Thr	Asn	Ala
			20					25					30		
Ile	Tyr	Gly	Phe	Val	Asn	Val	Ile	Leu	Lys	Tyr	Leu	Glu	Gln	Glu	Lys
		35					40					45			
Pro	Asp	Tyr	Val	Ala	Val	Ala	Phe	Asp	Lys	Arg	Gly	Arg	Glu	Ala	Arg
	50					55					60				
Lys	Ser	Glu	Tyr	Glu	Glu	Tyr	Lys	Ala	Asn	Arg	Lys	Pro	Met	Pro	Asp
65					70					75					80
Asn	Leu	Gln	Val	Gln	Ile	Pro	Tyr	Val	Arg	Glu	Ile	Leu	Tyr	Ala	Phe
				85					90					95	
Asn	Ile	Pro	Ile	Ile	Glu	Phe	Glu	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Ile
			100					105					110		
Gly	Ser	Leu	Val	Asn	Gln	Phe	Lys	Asn	Thr	Gly	Leu	Asp	Ile	Val	Ile
		115					120					125			
Ile	Thr	Gly	Asp	Arg	Asp	Thr	Leu	Gln	Leu	Leu	Asp	Lys	Asn	Val	Val
	130					135					140				
Val	Lys	Ile	Val	Ser	Thr	Lys	Phe	Asp	Lys	Thr	Val	Glu	Asp	Leu	Tyr
145					150					155					160
Thr	Val	Glu	Asn	Val	Lys	Glu	Lys	Tyr	Gly	Val	Trp	Ala	Asn	Gln	Val
				165					170					175	
Pro	Asp	Tyr	Lys	Ala	Leu	Val	Gly	Asp	Gln	Ser	Asp	Asn	Ile	Pro	Gly
			180					185					190		
Val	Lys	Gly	Ile	Gly	Glu	Lys	Ser	Ala	Gln	Lys	Leu	Leu	Glu	Glu	Tyr
		195					200					205			
Ser	Ser	Leu	Glu	Glu	Ile	Tyr	Gln	Asn	Leu	Asp	Lys	Ile	Lys	Ser	Ser
	210					215					220				
Ile	Arg	Glu	Lys	Leu	Glu	Ala	Gly	Lys	Asp	Met	Ala	Phe	Leu	Ser	Lys
225					230					235					240
Arg	Leu	Ala	Thr	Ile	Val	Cys	Asp	Leu	Pro	Leu	Asn	Val	Lys	Leu	Glu
				245					250					255	
Asp	Leu	Arg	Thr	Lys	Glu	Trp	Asn	Lys	Glu	Arg	Leu	Tyr	Glu	Ile	Leu
			260					265					270		
Val	Gln	Leu	Glu	Phe	Lys	Ser	Ile	Ile	Lys	Arg	Leu	Gly	Leu	Ser	Glu
		275					280					285			
Val	Val	Gln	Phe	Glu	Phe	Val	Gln	Gln	Arg	Thr	Asp	Ile	Pro	Asp	Val
	290					295					300				

Glu	Gln	Lys	Glu	Leu	Glu	Ser	Ile	Ser	Gln	Ile	Arg	Ser	Lys	Glu	Ile	305	310	315	320
Pro	Leu	Met	Phe	Val	Gln	Gly	Glu	Lys	Cys	Phe	Tyr	Leu	Tyr	Asp	Gln	325	330	335	
Glu	Ser	Asn	Thr	Val	Phe	Ile	Thr	Ser	Asn	Lys	Leu	Leu	Ile	Glu	Glu	340	345	350	
Ile	Leu	Lys	Ser	Asp	Thr	Val	Lys	Ile	Met	Tyr	Asp	Leu	Lys	Asn	Ile	355	360	365	
Phe	His	Gln	Leu	Asn	Leu	Glu	Asp	Thr	Asn	Asn	Ile	Lys	Asn	Cys	Glu	370	375	380	
Asp	Val	Met	Ile	Ala	Ser	Tyr	Val	Leu	Asp	Ser	Thr	Arg	Ser	Ser	Tyr	385	390	395	400
Glu	Leu	Glu	Thr	Leu	Phe	Val	Ser	Tyr	Leu	Asn	Thr	Asp	Ile	Glu	Ala	405	410		415
Val	Lys	Lys	Asp	Lys	Lys	Ile	Val	Ser	Val	Val	Leu	Leu	Lys	Arg	Leu	420	425	430	
Trp	Asp	Glu	Leu	Leu	Arg	Leu	Ile	Asp	Leu	Asn	Ser	Cys	Gln	Phe	Leu	435	440	445	
Tyr	Glu	Asn	Ile	Glu	Arg	Pro	Leu	Ile	Pro	Val	Leu	Tyr	Glu	Met	Glu	450	455	460	
Lys	Thr	Gly	Phe	Lys	Val	Asp	Arg	Asp	Ala	Leu	Ile	Gln	Tyr	Thr	Lys	465	470	475	480
Glu	Ile	Glu	Asn	Lys	Ile	Leu	Lys	Leu	Glu	Thr	Gln	Ile	Tyr	Gln	Ile	485	490		495
Ala	Gly	Glu	Trp	Phe	Asn	Ile	Asn	Ser	Pro	Lys	Gln	Leu	Ser	Tyr	Ile	500	505	510	
Leu	Phe	Glu	Lys	Leu	Lys	Leu	Pro	Val	Ile	Lys	Lys	Thr	Lys	Thr	Gly	515	520	525	
Tyr	Ser	Thr	Asp	Ala	Glu	Val	Leu	Glu	Glu	Leu	Phe	Asp	Lys	His	Glu	530	535	540	
Ile	Val	Pro	Leu	Ile	Leu	Asp	Tyr	Arg	Met	Tyr	Thr	Lys	Ile	Leu	Thr	545	550	555	560
Thr	Tyr	Cys	Gln	Gly	Leu	Leu	Gln	Ala	Ile	Asn	Pro	Ser	Ser	Gly	Arg	565	570	575	
Val	His	Thr	Thr	Phe	Ile	Gln	Thr	Gly	Thr	Ala	Thr	Gly	Arg	Leu	Ala	580	585	590	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Lys	Tyr	Asp	Glu	Gly	595	600	605	
Lys	Leu	Ile	Arg	Lys	Val	Phe	Val	Pro	Glu	Gly	Gly	His	Val	Leu	Ile	610	615	620	
Asp	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Leu	Ala	His	Ile	Ser	625	630	635	640

Glu Asp Glu Arg Leu Ile Ser Ala Phe Lys Asn Asn Val Asp Ile His  
 645 650 655  
 Ser Gln Thr Ala Ala Glu Val Phe Gly Val Asp Ile Ala Asp Val Thr  
 660 665 670  
 Pro Glu Met Arg Ser Gln Ala Lys Ala Val Asn Phe Gly Ile Val Tyr  
 675 685  
 Gly Ile Ser Asp Tyr Gly Leu Ala Arg Asp Ile Lys Ile Ser Arg Lys  
 690 695 700  
 Glu Ala Ala Glu Phe Ile Asn Lys Tyr Phe Glu Arg Tyr Pro Lys Val  
 705 710 715 720  
 Lys Glu Tyr Leu Asp Asn Thr Val Lys Phe Ala Arg Asp Asn Gly Phe  
 725 730 735  
 Val Leu Thr Leu Phe Asn Arg Lys Arg Tyr Ile Lys Asp Ile Lys Ser  
 740 745 750  
 Thr Asn Arg Asn Leu Arg Gly Tyr Ala Glu Arg Ile Ala Met Asn Ser  
 755 760 765  
 Pro Ile Gln Gly Ser Ala Ala Asp Ile Met Lys Leu Ala Met Ile Lys  
 770 775 780  
 Val Tyr Gln Lys Leu Lys Glu Asn Asn Leu Lys Ser Lys Ile Ile Leu  
 785 790 795 800  
 Gln Val His Asp Glu Leu Leu Ile Glu Ala Pro Tyr Glu Glu Lys Asp  
 805 810 815  
 Ile Val Lys Glu Ile Val Lys Arg Glu Met Glu Asn Ala Val Ala Leu  
 820 825 830  
 Lys Val Pro Leu Val Val Glu Val Lys Glu Gly Leu Asn Trp Tyr Glu  
 835 840 845  
 Asn Lys Ile  
 850

<210> 44  
 <211> 928  
 <212> PRT  
 <213> E. coli

<400> 44  
 Met Val Gln Ile Pro Gln Asn Pro Leu Ile Leu Val Asp Gly Ser Ser  
 1 5 10 15  
 Tyr Leu Tyr Arg Ala Tyr His Ala Phe Pro Pro Leu Thr Asn Ser Ala  
 20 25 30  
 Gly Glu Pro Thr Gly Ala Met Tyr Gly Val Leu Asn Met Leu Arg Ser  
 35 40 45  
 Leu Ile Met Gln Tyr Lys Pro Thr His Ala Ala Val Val Phe Asp Ala  
 50 55 60  
 Lys Gly Lys Thr Phe Arg Asp Glu Leu Phe Glu His Tyr Lys Ser His

65	70					75					80				
Arg	Pro	Pro	Met	Pro	Asp	Asp	Leu	Arg	Ala	Gln	Ile	Glu	Pro	Leu	His
				85					90					95	
Ala	Met	Val	Lys	Ala	Met	Gly	Leu	Pro	Leu	Leu	Ala	Val	Ser	Gly	Val
			100					105					110		
Glu	Ala	Asp	Asp	Val	Ile	Gly	Thr	Leu	Ala	Arg	Glu	Ala	Glu	Lys	Ala
		115					120					125			
Gly	Arg	Pro	Val	Leu	Ile	Ser	Thr	Gly	Asp	Lys	Asp	Met	Ala	Gln	Leu
	130					135					140				
Val	Thr	Pro	Asn	Ile	Thr	Leu	Ile	Asn	Thr	Met	Thr	Asn	Thr	Ile	Leu
145					150					155					160
Gly	Pro	Glu	Glu	Val	Val	Asn	Lys	Tyr	Gly	Val	Pro	Pro	Glu	Leu	Ile
				165					170					175	
Ile	Asp	Phe	Leu	Ala	Leu	Met	Gly	Asp	Ser	Ser	Asp	Asn	Ile	Pro	Gly
			180					185					190		
Val	Pro	Gly	Val	Gly	Glu	Lys	Thr	Ala	Gln	Ala	Leu	Leu	Gln	Gly	Leu
		195					200					205			
Gly	Gly	Leu	Asp	Thr	Leu	Tyr	Ala	Glu	Pro	Glu	Lys	Ile	Ala	Gly	Leu
	210					215					220				
Ser	Phe	Arg	Gly	Ala	Lys	Thr	Met	Ala	Ala	Lys	Leu	Glu	Gln	Asn	Lys
225					230					235					240
Glu	Val	Ala	Tyr	Leu	Ser	Tyr	Gln	Leu	Ala	Thr	Ile	Lys	Thr	Asp	Val
				245					250					255	
Glu	Leu	Glu	Leu	Thr	Cys	Glu	Gln	Leu	Glu	Val	Gln	Gln	Pro	Ala	Ala
			260					265					270		
Glu	Glu	Leu	Leu	Gly	Leu	Phe	Lys	Lys	Tyr	Glu	Phe	Lys	Arg	Trp	Thr
		275					280					285			
Ala	Asp	Val	Glu	Ala	Gly	Lys	Trp	Leu	Gln	Ala	Lys	Gly	Ala	Lys	Pro
	290					295					300				
Ala	Ala	Lys	Pro	Gln	Glu	Thr	Ser	Val	Ala	Asp	Glu	Ala	Pro	Glu	Val
305					310					315					320
Thr	Ala	Thr	Val	Ile	Ser	Tyr	Asp	Asn	Tyr	Val	Thr	Ile	Leu	Asp	Glu
				325					330					335	
Glu	Thr	Leu	Lys	Ala	Trp	Ile	Ala	Lys	Leu	Glu	Lys	Ala	Pro	Val	Phe
			340					345					350		
Ala	Phe	Asp	Thr	Glu	Thr	Asp	Ser	Leu	Asp	Asn	Ile	Ser	Ala	Asn	Leu
		355					360					365			
Val	Gly	Leu	Ser	Phe	Ala	Ile	Glu	Pro	Gly	Val	Ala	Ala	Tyr	Ile	Pro
	370					375					380				
Val	Ala	His	Asp	Tyr	Leu	Asp	Ala	Pro	Asp	Gln	Ile	Ser	Arg	Glu	Arg
385					390					395					400

Ala	Leu	Glu	Leu	Leu	Lys	Pro	Leu	Leu	Glu	Asp	Glu	Lys	Ala	Leu	Lys	
				405					410						415	
Val	Gly	Gln	Asn	Leu	Lys	Tyr	Asp	Arg	Gly	Ile	Leu	Ala	Asn	Tyr	Gly	
			420					425					430			
Ile	Glu	Leu	Arg	Gly	Ile	Ala	Phe	Asp	Thr	Met	Leu	Glu	Ser	Tyr	Ile	
		435					440					445				
Leu	Asn	Ser	Val	Ala	Gly	Arg	His	Asp	Met	Asp	Ser	Leu	Ala	Glu	Arg	
	450					455					460					
Trp	Leu	Lys	His	Lys	Thr	Ile	Thr	Phe	Glu	Glu	Ile	Ala	Gly	Lys	Gly	
465					470					475					480	
Lys	Asn	Gln	Leu	Thr	Phe	Asn	Gln	Ile	Ala	Leu	Glu	Glu	Ala	Gly	Arg	
				485					490					495		
Tyr	Ala	Ala	Glu	Asp	Ala	Asp	Val	Thr	Leu	Gln	Leu	His	Leu	Lys	Met	
			500					505					510			
Trp	Pro	Asp	Leu	Gln	Lys	His	Lys	Gly	Pro	Leu	Asn	Val	Phe	Glu	Asn	
		515					520					525				
Ile	Glu	Met	Pro	Leu	Val	Pro	Val	Leu	Ser	Arg	Ile	Glu	Arg	Asn	Gly	
	530					535					540					
Val	Lys	Ile	Asp	Pro	Lys	Val	Leu	His	Asn	His	Ser	Glu	Glu	Leu	Thr	
545					550					555					560	
Leu	Arg	Leu	Ala	Glu	Leu	Glu	Lys	Lys	Ala	His	Glu	Ile	Ala	Gly	Glu	
				565					570					575		
Glu	Phe	Asn	Leu	Ser	Ser	Thr	Lys	Gln	Leu	Gln	Thr	Ile	Leu	Phe	Glu	
			580					585					590			
Lys	Gln	Gly	Ile	Lys	Pro	Leu	Lys	Lys	Thr	Pro	Gly	Gly	Ala	Pro	Ser	
		595					600					605				
Thr	Ser	Glu	Glu	Val	Leu	Glu	Glu	Leu	Ala	Leu	Asp	Tyr	Pro	Leu	Pro	
	610					615					620					
Lys	Val	Ile	Leu	Glu	Tyr	Arg	Gly	Leu	Ala	Lys	Leu	Lys	Ser	Thr	Tyr	
625					630					635					640	
Thr	Asp	Lys	Leu	Pro	Leu	Met	Ile	Asn	Pro	Lys	Thr	Gly	Arg	Val	His	
				645					650					655		
Thr	Ser	Tyr	His	Gln	Ala	Val	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Thr	
			660					665					670			
Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Asn	Glu	Glu	Gly	Arg	Arg	
		675					680					685				
Ile	Arg	Gln	Ala	Phe	Ile	Ala	Pro	Glu	Asp	Tyr	Val	Ile	Val	Ser	Ala	
	690					695					700					
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Ile	Met	Ala	His	Leu	Ser	Arg	Asp	
705					710					715					720	
Lys	Gly	Leu	Leu	Thr	Ala	Phe	Ala	Glu	Gly	Lys	Asp	Ile	His	Arg	Ala	
				725					730					735		



Thr	Ala	Ala	Glu	Val	Phe	Gly	Leu	Pro	Leu	Glu	Thr	Val	Thr	Ser	Glu	740	745	750
Gln	Arg	Arg	Ser	Ala	Lys	Ala	Ile	Asn	Phe	Gly	Leu	Ile	Tyr	Gly	Met	755	760	765
Ser	Ala	Phe	Gly	Leu	Ala	Arg	Gln	Leu	Asn	Ile	Pro	Arg	Lys	Glu	Ala	770	775	780
Gln	Lys	Tyr	Met	Asp	Leu	Tyr	Phe	Glu	Arg	Tyr	Pro	Gly	Val	Leu	Glu	785	790	795
Tyr	Met	Glu	Arg	Thr	Arg	Ala	Gln	Ala	Lys	Glu	Gln	Gly	Tyr	Val	Glu	805	810	815
Thr	Leu	Asp	Gly	Arg	Arg	Leu	Tyr	Leu	Pro	Asp	Ile	Lys	Ser	Ser	Asn	820	825	830
Gly	Ala	Arg	Arg	Ala	Ala	Ala	Glu	Arg	Ala	Ala	Ile	Asn	Ala	Pro	Met	835	840	845
Gln	Gly	Thr	Ala	Ala	Asp	Ile	Ile	Lys	Arg	Ala	Met	Ile	Ala	Val	Asp	850	855	860
Ala	Trp	Leu	Gln	Ala	Glu	Gln	Pro	Arg	Val	Arg	Met	Ile	Met	Gln	Val	865	870	875
His	Asp	Glu	Leu	Val	Phe	Glu	Val	His	Lys	Asp	Asp	Val	Asp	Ala	Val	885	890	895
Ala	Lys	Gln	Ile	His	Gln	Leu	Met	Glu	Asn	Cys	Thr	Arg	Leu	Asp	Val	900	905	910
Pro	Leu	Leu	Val	Glu	Val	Gly	Ser	Gly	Glu	Asn	Trp	Asp	Gln	Ala	His	915	920	925